

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/677,956A
Source: IFW/6
Date Processed by STIC: 07/07/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/07/2006

PATENT APPLICATION: US/10/677,956A

TIME: 17:08:11

Input Set : A:\323-100USD.ST25.txt

Output Set: N:\CRF4\07072006\J677956A.raw

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5 <110> APPLICANT: Zebedee, Suzanne
6     Inchauspe, Genevieve
7     Nasoff, Marc S.
8     Prince, Alfred M.
10 <120> TITLE OF INVENTION: METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT VIRAL ANTIGENS
12 <130> FILE REFERENCE: 323-100USD
14 <140> CURRENT APPLICATION NUMBER: 10/677,956A
15 <141> CURRENT FILING DATE: 2003-10-01
17 <150> PRIOR APPLICATION NUMBER: 08/931,855
18 <151> PRIOR FILING DATE: 1997-09-16
20 <150> PRIOR APPLICATION NUMBER: 08/563,733
21 <151> PRIOR FILING DATE: 1995-11-08
23 <150> PRIOR APPLICATION NUMBER: 08/272,271
24 <151> PRIOR FILING DATE: 1994-07-08
26 <150> PRIOR APPLICATION NUMBER: 07/616,369
27 <151> PRIOR FILING DATE: 1990-11-21
29 <150> PRIOR APPLICATION NUMBER: 07/573,643
30 <151> PRIOR FILING DATE: 1990-08-27
32 <160> NUMBER OF SEQ ID NOS: 71
34 <170> SOFTWARE: PatentIn version 3.3
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 795
38 <212> TYPE: DNA
39 <213> ORGANISM: Human immunodeficiency virus
42 <220> FEATURE:
43 <221> NAME/KEY: CDS
44 <222> LOCATION: (16)..(789)
46 <400> SEQUENCE: 1
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48           Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
49           1             5             10
51 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
52 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
53           15             20             25
55 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta      147
56 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
57           30             35             40
59 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg      195
60 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
61 45             50             55             60
63 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag      243
64 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
65           65             70             75

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67 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att      291
68 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
69          80          85          90
71 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act      339
72 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
73          95          100          105
75 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct      387
76 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
77          110          115          120
79 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat      435
80 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
81 125          130          135          140
83 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa      483
84 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
85          145          150          155
87 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act      531
88 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
89          160          165          170
91 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa      579
92 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
93          175          180          185
95 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa      627
96 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
97          190          195          200
99 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag      675
100 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
101 205          210          215          220
103 gga gta gga gga ccc aaa aat caa caa tta tta tcc tta tgg ggg tgt      723
104 Gly Val Gly Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys
105          225          230          235
107 aaa ggg aaa ctt gtt tgt tat act tcc gtt aaa tgg aat gga ccc ggc      771
108 Lys Gly Lys Leu Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
109          240          245          250
111 cat aag gca aga gtt ttg taataa      795
112 His Lys Ala Arg Val Leu
113          255
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117 <211> LENGTH: 258
118 <212> TYPE: PRT
119 <213> ORGANISM: Human immunodeficiency virus
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128          20          25          30
131 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
132          35          40          45
135 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
136          50          55          60

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139 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
140 65              70              75              80
143 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
144              85              90              95
147 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
148              100             105             110
151 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
152              115             120             125
155 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
156              130             135             140
159 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
160 145             150             155             160
163 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
164              165             170             175
167 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
168              180             185             190
171 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
172              195             200             205
175 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
176              210             215             220
179 Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu
180 225             230             235             240
183 Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg
184              245             250             255
187 Val Leu
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192 <211> LENGTH: 795
193 <212> TYPE: DNA
194 <213> ORGANISM: Human immunodeficiency virus
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (16)..(789)
201 <400> SEQUENCE: 3
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204              1              5              10
206 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
207 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
208              15              20              25
210 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta      147
211 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
212              30              35              40
214 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg      195
215 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
216 45              50              55              60
218 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag      243
219 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
220              65              70              75
222 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att      291

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223 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
224      80      85      90
226 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act      339
227 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
228      95      100      105
230 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct      387
231 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
232      110      115      120
234 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat      435
235 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
236 125      130      135      140
238 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa      483
239 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
240      145      150      155
242 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act      531
243 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
244      160      165      170
246 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa      579
247 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
248      175      180      185
250 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa      627
251 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
252      190      195      200
254 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag      675
255 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
256 205      210      215      220
258 gga gta gga gga ccc aaa aat caa caa aga tta aat tta tgg ggg tgt      723
259 Gly Val Gly Gly Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys
260      225      230      235
262 aaa ggg aaa ctt att tgt tat act tcc gtt aaa tgg aat gga ccc ggc      771
263 Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
264      240      245      250
266 cat aag gca aga gtt ttg taataa      795
267 His Lys Ala Arg Val Leu
268      255
271 <210> SEQ ID NO: 4
272 <211> LENGTH: 258
273 <212> TYPE: PRT
274 <213> ORGANISM: Human immunodeficiency virus
276 <400> SEQUENCE: 4
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279 1      5      10      15
282 Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala
283      20      25      30
286 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
287      35      40      45
290 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
291      50      55      60
294 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu

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295 65              70              75              80
298 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
299              85              90              95
302 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
303              100              105              110
306 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
307              115              120              125
310 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
311              130              135              140
314 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
315 145              150              155              160
318 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
319              165              170              175
322 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
323              180              185              190
326 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
327              195              200              205
330 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
331              210              215              220
334 Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu
335 225              230              235              240
338 Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg
339              245              250              255
342 Val Leu
346 <210> SEQ ID NO: 5
347 <211> LENGTH: 795
348 <212> TYPE: DNA
349 <213> ORGANISM: Human immunodeficiency virus
352 <220> FEATURE:
353 <221> NAME/KEY: CDS
354 <222> LOCATION: (16)..(789)
356 <400> SEQUENCE: 5
357 aggagggttt ttcat atg cca atc gtg cag aac atc cag ggg caa atg gta      51
358              Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
359              1              5              10
361 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
362 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
363              15              20              25
365 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta      147
366 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
367              30              35              40
369 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg      195
370 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
371 45              50              55              60
373 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag      243
374 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
375              65              70              75
377 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att      291
378 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/07/2006
PATENT APPLICATION: US/10/677,956A TIME: 17:08:12

Input Set : A:\323-100USD.ST25.txt
Output Set: N:\CRF4\07072006\J677956A.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:68,69,70,71

VERIFICATION SUMMARY

DATE: 07/07/2006

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Input Set : A:\323-100USD.ST25.txt

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